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By Elisa Goodrich

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

17169/04

In re the Application of	
Thompson, G., et al.	Serial No. 07/762,762
Examiner: Leguyader, J.	Allowed: August 2, 1999
Filed: September 16, 1991	Batch No.: W48
For: PLANT DESATURASES COMPOSITIONS AND USES	SUBMISSION OF SUBSTITUTE DRAWINGS UNDER 37 CFR 1.84

Honorable Commissioner of
Patents and Trademarks
Washington, DC 20231

OFFICIAL DRAFTSMAN

Dear Sir:

This letter is in response to the Draftsmen's comments mailed on August 2, 1999 objecting to the drawings as submitted by Applicants in a communication of September 16, 1991. Provided herewith are substitute drawings for Figure 1-10. The substitute drawings are in compliance with the requirements for formal drawings made in this case under 37 CFR § 1.84.

No substantial modifications have been made to these substitute drawings.

A conditional petition for an Extension of Time is requested to provide for the timely filing if an extension of time is required after all papers filed with this transmittal have been considered.

The Commissioner is GENERALLY authorized to charge any required fees, with the exception of an Issue Fee, relating to this paper to Deposit Account No. 03-0173.

In the event that there are any questions regarding these Figures, the Draftsman is invited to contact the undersigned at (530) 753-6313.

Respectfully submitted,

Carl J. Schwedler
Reg. No. 36,924

CALGENE LLC
1920 Fifth Street
Davis, CA 95616
(530) 753-6313

Enclosure: Figures 1-10

ASTLGSSTPKVDNAKKPFQPPREVHVQVTH$^{S}_{X}$ MPPQKIEIFKSIEG$^{W}_{R}$ AEQNILV$^{H}_{F}$ LKPVEKCWQ

F2: DFLPDPA$^{S}_{T}$ EGFDEQVKELRARAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGV

F3: DETGASLTPWAVWT

F4: DLLHTYLYLSGRV

F5: DMRQIQKTIQYLI

F6: TENSPYLGFIYTSFQER

F7: DV$^{K}_{F}$ LAQI$^{C}_{Q}$ GTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI$^{S}_{T}$ MPAHLMY

F8: DNLF

F9: dvFlAV$^{A}_{I}$ QRL$^{G}_{I}$ VYTAK

F10: DYADILEFLVGRWK

F11: VADLTGLSGEGRKAQA$^{Q}_{G}$ DYVCGLPPRIRRLEERAQGRAKEGPVVPFSWIFDRQVKL

FIGURE 1


HindIII
1 GCTCACTTGTGTGGTGGAGGAGAAAAACAGAACTCACAAAAAGCTTTGCGACTGCCAAGAACAACAACA
69
42
70 ACAACAAGATCAAGAAGAAGAAGAAGAAGATCAAAAATGGCTCTTCGAATCACTCCAGTGACCTTGCAA
138
METAlaLeuArgIleThrProValThrLeuGln
EcoRV
BglII
NcoI
139 TCGGAGAGATATCGTTCGTTTTCGTTTCCTAAGAAGGCTAATCTCAGATCTCCCAAATTCGCCATGGCC
207
SerGluArgTyrArgSerPheSerPheProLysLysAlaAsnLeuArgSerProLysPheAlaMETAla
149
185
201
HindII
208 TCCACCCTCGGATCATCCACACCGAAGGTTGACAATGCCAAGAAGCCTTTTCAACCTCCACGAGAGGTT
276
SerThrLeuGlySerSerThrProLysValAspAsnAlaLysLysProPheGlnProProArgGluVal
238
277 CATGTTCAGGTGACGCACTCCATGCCACCACAGAAGATAGAGATTTTCAAATCCATCGAGGGTTGGGCT
345
HisValGlnValThrHisSerMETProProGlnLysIleGluIlePheLysSerIleGluGlyTrpAla

FIGURE 2

```
 346 GAGCAGAACATATTGGTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGCACAGGATTTCTTGCCGGAC
414
     GluGlnAsnIleLeuValHisLeuLysProValGluLysCysTrpGlnAlaGlnAspPheLeuProAsp
```

FIGURE 2


415 CCTGCATCTGAAGGATTTGATGAACAAGTCAAGGAACTAAGGGCAAGAGCAAAGGAGATTCCTGATGAT
483
ProAlaSerGluGlyPheAspGluGlnValLysGluLeuArgAlaArgAlaLysGluIleProAspAsp
484 TACTTTGTTGTTTTGGTTGGAGATATGATTACAGAGGAAGCCCTACCTACTTACCAAACAATGCTTAAT
552
TyrPheValValLeuValGlyAspMETIleThrGluGluAlaLeuProThrTyrGlnThrMETLeuAsn
553 ACCCTAGATGGTGTACGTGATGAGACTGGGGCTAGCCTTACGCCTTGGGCTGTCTGGACTAGGGCTTGG
621
ThrLeuAspGlyValArgAspGluThrGlyAlaSerLeuThrProTrpAlaValTrpThrArgAlaTrp
PvuII
AccI
622 ACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACCTATCTCTACCTTTCTGGGCGGGTAGACATG
690
ThrAlaGluGluAsnArgHisGlyAspLeuLeuHisThrTyrLeuTyrLeuSerGlyArgValAspMET
626
684
BamHI
691 AGGCAGATACAGAAGACAATTCAGTATCTCATTGGGTCAGGAATGGATCCTCGTACCGAAAACAGCCCC
759
ArgGlnIleGlnLysThrIleGlnTyrLeuIleGlySerGlyMETAspProArgThrGluAsnSerPro
736

FIGURE 2

760 TACCTTGGGTTCATCTACACATCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAAACACCGCCAGG
828

TyrLeuGlyPheIleTyrThrSerPheGlnGluArgAlaThrPheValSerHisGlyAsnThrAlaArg

FIGURE 2

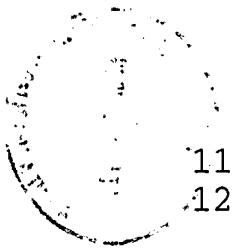

SphI
829 CATGCAAAGGATCATGGGGACGTGAAACTGGCGCAAATTTGTGGTACAATCGCGTCTGACGAAAAGCGT
897
HisAlaLysAspHisGlyAspValLysLeuAlaGlnIleCysGlyThrIleAlaSerAspGluLysArg
833
ClaI
898 CACGAGACCGCTTATACAAAGATAGTCGAAAAGCTATTCGAGATCGATCCTGATGGCACCGTTCTTGCT
966
HisGluThrAlaTyrThrLysIleValGluLysLeuPheGluIleAspProAspGlyThrValLeuAla
942
BglII
967 TTTGCCGACATGATGAGGAAAAAGATCTCGATGCCCGCACACTTGATGTACGATGGGCGTGATGACAAC
1035
PheAlaAspMETMETArgLysLysIleSerMETProAlaHisLeuMETTyrAspGlyArgAspAspAsn
990
AccI
1036 CTCTTCGAACATTTCTCGGCGGTTGCCCAAAGACTCGGCGTCTACACCGCCAAAGACTACGCCGACATA
1104
LeuPheGluHisPheSerAlaValAlaGlnArgLeuGlyValTyrThrAlaLysAspTyrAlaAspIle
1077

FIGURE 2

1105 CTGGAATTTCTGGTCGGGCGGTGGAAAGTGGCGGATTTGACCGGCCTATCTGGTGAAGGGCGTAAAGCG
1173

LeuGluPheLeuValGlyArgTrpLysValAlaAspLeuThrGlyLeuSerGlyGluGlyArgLysAla

FIGURE 2



SacI

1174 CAAGATTATGTTTGCGGGTTGCCACCAAGAATCAGAAGGCTGGAGGAGAGAGCTCAAGGGCGAGCAAAG
1242

GlnAspTyrValCysGlyLeuProProArgIleArgArgLeuGluGluArgAlaGlnGlyArgAlaLys
1228

PvuII

1243 GAAGGACCTGTTGTTCCATTCAGCTGGATTTTCGATAGACAGGTGAAGCTGTGAAGAAAAAAAAAAACGA
1311

GluGlyProValValProPheSerTrpIlePheAspArgGlnValLysLeu
1266

1312 GCAGTGAGTTCGGTTTCTGTTGGCTTATTGGGTAGAGGTTAAAACCTATTTTAGATGTCTGTTTCGTGT
1380

1381 AATGTGGTTTTTTTTCTTCTAATCTTGAATCTGGTATTGTGTCGTTGAGTTCGCGTGTGTGTAAACTTG
1449

1450 TGTGGCTGTGGACATATTATAGAACTCGTTATGCCAATTTTGATGACGGTGGTTATCGTCTCCCCTGGT
1518

1519 GTTTTTTTATTGTTT 1533

FIGURE 2

```
AAAAGAAAAA GGTAAGAAAA AAAACA ATG GCT CTC AAG CTC AAT CCT TTC CTT TCT          56
                             MET Ala Leu Lys Leu Asn Pro Phe Leu Ser

CAA ACC CAA AAG TTA CCT TCT TTC GCT CTT CCA CCA ATG GCC AGT ACC AGA TCT      110
Gln Thr Gln Lys Leu Pro Ser Phe Ala Leu Pro Pro MET Ala Ser Thr Arg Ser

CCT AAG TTC TAC ATG GCC TCT ACC CTC AAG TCT GGT TCT AAG GAA GTT GAG AAT      164
Pro Lys Phe Tyr MET Ala Ser Thr Leu Lys Ser Gly Ser Lys Glu Val Glu Asn

CTC AAG AAG CCT TTC ATG CCT CCT CGG GAG GTA CAT GTT CAG GTT ACC CAT TCT      218
Leu Lys Lys Pro Phe MET Pro Pro Arg Glu Val His Val Gln Val Thr His Ser

ATG CCA CCC CAA AAG ATT GAG ATC TTT AAA TCC CTA GAC AAT TGG GCT GAG GAG      272
MET Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Asp Asn Trp Ala Glu Glu

AAC ATT CTG GTT CAT CTG AAG CCA GTT GAG AAA TGT TGG CAA CCG CAG GAT TTT      326
Asn Ile Leu Val His Leu Lys Pro Val Glu Lys Cys Trp Gln Pro Gln Asp Phe

TTG CCA GAT CCC GCC TCT GAT GGA TTT GAT GAG CAA GTC AGG GAA CTC AGG GAG      380
Leu Pro Asp Pro Ala Ser Asp Gly Phe Asp Glu Gln Val Arg Glu Leu Arg Glu

AGA GCA AAG GAG ATT CCT GAT GAT TAT TTT GTT GTT TTG GTT GGA GAC ATG ATA      434
Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile

ACG GAA GAA GCC CTT CCC ACT TAT CAA ACA ATG CTG AAT ACC TTG GAT GGA GTT      488
Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val
```

FIGURE 3B
1 of 3

```
CGG GAT GAA ACA GGT GCA AGT CCT ACT TCT TGG GCA ATT TGG ACA AGG GCA TGG        542
Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp

ACT GCG GAA GAG AAT AGA CAT GGT GAC CTC CTC AAT AAG TAT CTC TAC CTA TCT        596
Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser

GGA CGA GTG GAC ATG AGG CAA ATT GAG AAG ACA ATT CAA TAT TTG ATT GGT TCA        650
Gly Arg Val Asp MET Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser

GGA ATG GAT CCA CGG ACA GAA AAC AGT CCA TAC CTT GGG TTC ATC TAT ACA TCA        704
Gly MET Asp Pro Arg Thr Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser

TTC CAG GAA AGG GCA ACC TTC ATT TCT CAT GGG AAC ACT GCC CGA CAA GCC AAA        758
Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys

GAG CAT GGA GAC ATA AAG TTG GCT CAA ATA TGT GGT ACA ATT GCT GCA GAT GAG        812
Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu

AAG CGC CAT GAG ACA GCC TAC ACA AAG ATA GTG GAA AAA CTC TTT GAG ATT GAT        866
Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp

CCT GAT GGA ACT GTT TTG GCT TTT GCT GAT ATG ATG AGA AAG AAA ATT TCT ATG        920
Pro Asp Gly Thr Val Leu Ala Phe Ala Asp MET MET Arg Lys Lys Ile Ser MET

CCT GCA CAC TTG ATG TAT GAT GGC CGA GAT GAT AAT CTT TTT GAC CAC TTT TCA        974
Pro Ala His Leu MET Tyr Asp Gly Arg Asp Asp Asn Leu Phe Asp His Phe Ser
```

FIGURE 3B
2 of 3

```
GCT GTT GCG CAG CGT CTT GGA GTC TAC ACA GCA AAG GAT TAT GCA GAT ATA TTG       1028
Ala Val Ala Gln Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu

GAG TTC TTG GTG GGC AGA TGG AAG GTG GAT AAA CTA ACG GGC CTT TCA GCT GAG       1082
Glu Phe Leu Val Gly Arg Trp Lys Val Asp Lys Leu Thr Gly Leu Ser Ala Glu

GGA CAA AAG GCT CAG GAC TAT GTT TGT CGG TTA CCT CCA AGA ATT AGA AGG CTG       1136
Gly Gln Lys Ala Gln Asp Tyr Val Cys Arg Leu Pro Pro Arg Ile Arg Arg Leu

GAA GAG AGA GCT CAA GGA AGG GCA AAG GAA GCA CCC ACC ATG CCT TTC AGC TGG       1190
Glu Glu Arg Ala Gln Gly Arg Ala Lys Glu Ala Pro Thr MET Pro Phe Ser Trp

ATT TTC GAT AGG CAA GTG AAG CTG TAGGTGGCTA AAGTGCAGGA CGAAACCGAA ATGGTTAGTT   1254
Ile Phe Asp Arg Gln Val Lys Leu

TCACTCTTTT TCATGCCCAT CCCTGCAGAA TCAGAAGTAG AGGTAGAATT TTGTAGTTGC TTTTTTATTA  1324

CAAGTCCAGT TTAGTTTAAG GTCTGTGGAA GGGAGTTAGT TGAGGAGTGA ATTTAGTAAG TTGTAGATAC  1394

AGTTGTTTCT TGTGTTGTCA TGAGTATGCT GATAGAGAGC AGCTGTAGTT TTGTTGTTGT GTTCTTTTAT  1464

ATGGTCTCTT GTATGAGTTT CTTTTCTTTC CTTTTCTTCT TTCCTTTCCT CTCTCTCTCT CTCTCTCTCT  1534

CTCTTTTTCT CTTATCCCAA GTGTCTCAAG TATAATAAGC AAACGATCCA TGTGGCAATT TTGATGATGG  1604

TGATCAGTCT CACAACTTGA TCTTTTGTCT TCTATTGGAA ACACAGCCTG CTTGTTTGAA AAAA       1668
```

FIGURE 3B
3 of 3

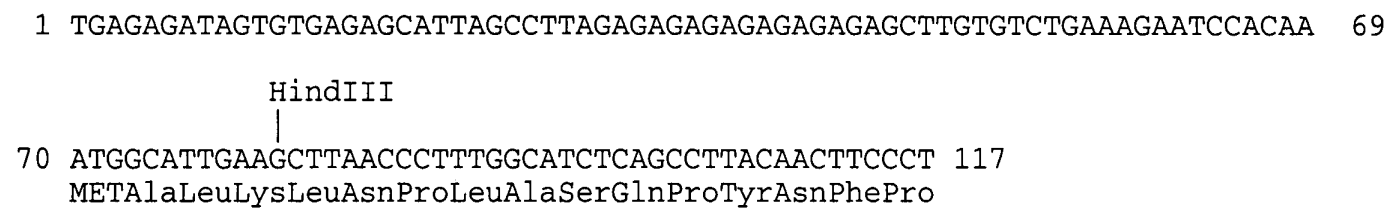

1 TGAGAGATAGTGTGAGAGCATTAGCCTTAGAGAGAGAGAGAGAGAGCTTGTGTCTGAAAGAATCCACAA 69
HindIII
70 ATGGCATTGAAGCTTAACCCTTTGGCATCTCAGCCTTACAACTTCCCT 117
METAlaLeuLysLeuAsnProLeuAlaSerGlnProTyrAsnPhePro

FIGURE 4A

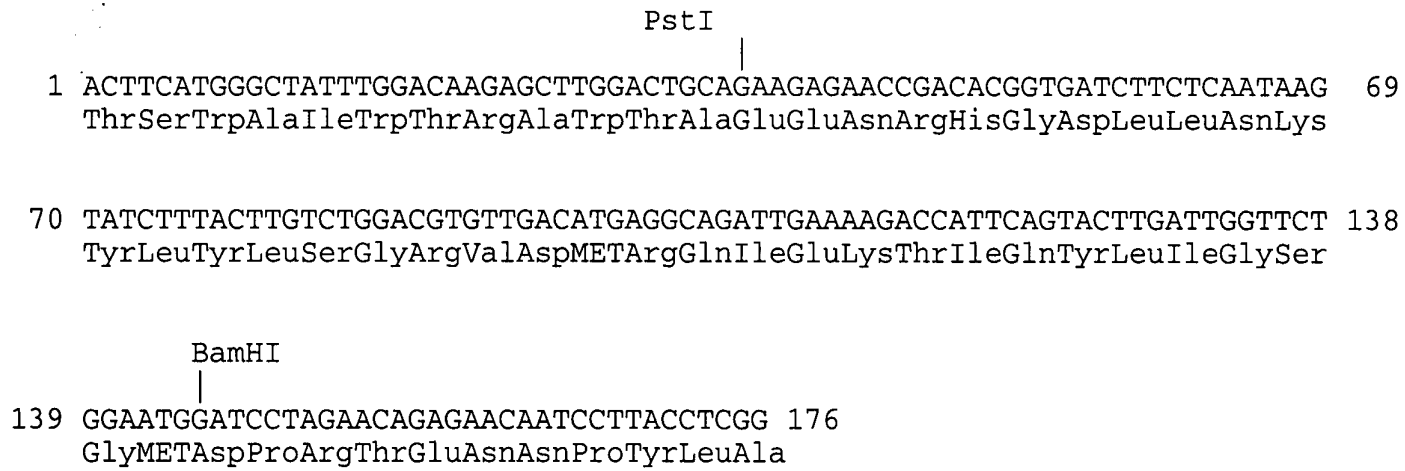

PstI
1 ACTTCATGGGCTATTTGGACAAGAGCTTGGACTGCAGAAGAGAACCGACACGGTGATCTTCTCAATAAG 69
ThrSerTrpAlaIleTrpThrArgAlaTrpThrAlaGluGluAsnArgHisGlyAspLeuLeuAsnLys
70 TATCTTTACTTGTCTGGACGTGTTGACATGAGGCAGATTGAAAAGACCATTCAGTACTTGATTGGTTCT 138
TyrLeuTyrLeuSerGlyArgValAspMETArgGlnIleGluLysThrIleGlnTyrLeuIleGlySer
BamHI
139 GGAATGGATCCTAGAACAGAGAACAATCCTTACCTCGG 176
GlyMETAspProArgThrGluAsnAsnProTyrLeuAla

FIGURE 4B

```
TGAGAGATAG TGTGAGAGCA TTAGCCTTAG AGAGAGAGAG AGAGAGCTTG TGTCTGAAAG AATCCACAA

ATG GCA TTG AAG CTT AAC CCT TTG GCA TCT CAG CCT TAC AAC TTC CCT TCC TCG
MET Ala Leu Lys Leu Asn Pro Leu Ala Ser Gln Pro Tyr Asn Phe Pro Ser Ser

GCT CGT CCG CCA ATC TCT ACT TTC AGA TCT CCC AAG TTC CTC TGC CTC GCT TCT
Ala Arg Pro Pro Ile Ser Thr Phe Arg Ser Pro Lys Phe Leu Cys Leu Ala Ser

TCT TCT CCC GCT CTC AGC TCC AAG GAG GTT GAG AGT TTG AAG AAG CCA TTC ACA
Ser Ser Pro Ala Leu Ser Ser Lys Glu Val Glu Ser Leu Lys Lys Pro Phe Thr

CCA CCT AAG GAA GTG CAC GTT CAA GTC CTG CAT TCC ATG CCA CCC CAG AAG ATC
Pro Pro Lys Glu Val His Val Gln Val Leu His Ser MET Pro Pro Gln Lys Ile

GAG ATC TTC AAA TCC ATG GAA GAC TGG GCC GAG CAG AAC CTT CTA ACT CAG CTC
Glu Ile Phe Lys Ser MET Glu Asp Trp Ala Glu Gln Asn Leu Leu Thr Gln Leu

AAA GAC GTG GAG AAG TCG TGG CAG CCC CAG GAC TTC TTA CCC GAC CCT GCA TCC
Lys Asp Val Glu Lys Ser Trp Gln Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser

GAT GGG TTC GAA GAT CAG GTT AGA GAG CTA AGA GAG AGG GCA AGA GAG CTC CCT
Asp Gly Phe Glu Asp Gln Val Arg Glu Leu Arg Glu Arg Ala Arg Glu Leu Pro

GAT GAT TAC TTC GTT GTT CTG GTG GGA GAC ATG ATC ACG GAA GAG GCG CTT CCG
Asp Asp Tyr Phe Val Val Leu Val Gly Asp MET Ile Thr Glu Glu Ala Leu Pro
```

FIGURE 4C
1 of 3

```
ACC TAT CAA ACC ATG TTG AAC ACT TTG GAT GGA GTG AGG GAT GAA ACT GGC GCT
Thr Tyr Gln Thr MET Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala

AGC CCC ACT TCA TGG GCT ATT TGG ACA AGA GCT TGG ACT GCA GAA GAG AAC CGA
Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg

CAC GGT GAT CTT CTC AAT AAG TAT CTT TAC TTG TCT GGA CGT GTT GAC ATG AGG
His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp MET Arg

CAG ATT GAA AAG ACC ATT CAG TAC TTG ATT GGT TCT GGA ATG GAT CCT AGA ACA
Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly MET Asp Pro Arg Thr

GAG AAC AAT CCT TAC CTC GGC TTC ATC TAC ACT TCA TTC CAA GAA AGA GCC ACC
Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr

TTC ATC TCT CAC GGA AAC ACA GCT CGC CAA GCC AAA GAG CAC GGA GAC CTC AAG
Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys Glu His Gly Asp Leu Lys

CTA GCC CAA ATC TGC GGC ACA ATA GCT GCA GAC GAG AAG CGT CAT GAG ACA GCT
Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala

TAC ACC AAG ATA GTT GAG AAG CTC TTT GAG ATT GAT CCT GAT GGT ACT GTG ATG
Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val MET

GCG TTT GCA GAC ATG ATG AGG AAG AAA ATC TCG ATG CCT GCT CAC TTG ATG TAC
Ala Phe Ala Asp MET MET Arg Lys Lys Ile Ser MET Pro Ala His Leu MET Tyr
```

FIGURE 4C
2 of 3

```
GAT GGG CGG GAT GAA AGC CTC TTT GAC AAC TTC TCT TCT GTT GCT CAG AGG CTC
Asp Gly Arg Asp Glu Ser Leu Phe Asp Asn Phe Ser Ser Val Ala Gln Arg Leu

GGT GTT TAC ACT GCC AAA GAC TAT GCG GAC ATT CTT GAG TTT TTG GTT GGG AGG
Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg

TGG AAG ATT GAG AGC TTG ACC GGG CTT TCA GGT GAA GGA AAC AAA GCG CAA GAG
Trp Lys Ile Glu Ser Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys Ala Gln Glu

TAC TTG TGT GGG TTG ACT CCA AGA ATC AGG AGG TTG GAT GAG AGA GCT CAA GCA
Tyr Leu Cys Gly Leu Thr Pro Arg Ile Arg Arg Leu Asp Glu Arg Ala Gln Ala

AGA GCC AAG AAA GGA CCC AAG GTT CCT TTC AGC TGG ATA CAT GAC AGA GAA GTG
Arg Ala Lys Lys Gly Pro Lys Val Pro Phe Ser Trp Ile His Asp Arg Glu Val

CAG CTC TAA AAAGGAA CAAAGCTATG AAACCTTTTC ACTCTCCGTC GTCCCTCATT TGATCTATCT
Gln Leu  *

GCTCTTGAAA TTGGTGTAGA TTACTATGGT TTGTGATATT GTTCGTGGGT CTAGTTACAA AGTTGAGAAG

CAGTGATTTA GTAGCTTTGT TGTTTCCAGT CTTTAAATGT TTTTGTGTTT GGTCCTTTTA GTAAACTTGT

TGTAGTTAAA TCAGTTGAAC TGTTTGGTCT GT
```

FIGURE 4C
3 of 3

```
GAT GCC AAA ANG CCT CAC ATG CCT CCT AGA GAA GCT CAT GTG CAA AAG   48
Asp Ala Lys Xaa Pro His MET Pro Pro Arg Glu Ala His Val Gln Lys
 1               5                  10                  15

ACC CAT TCA ATK CCG CCT CAA AAG ATT GAG ATT TTC AAA TCC TTG GAG   96
Thr His Ser Xaa Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Leu Glu
            20                  25                  30

GGT TGG GCT GAG GAG AAT GTC TTG GTG CAT CTT AAA CCT GTG GAG AA   143
Gly Trp Ala Glu Glu Asn Val Leu Val His Leu Lys Pro Val Glu
        35                  40                  45
```

FIGURE 5

Amino Acid Sequence From Fragment F2

K E I P D D Y FVVLVGDMITEEALPTY Q T M L N T

AAA GAA AUU CCN GAU GAU UAU CAA ACN AUG CUN AAU AC/N
G G C C C C G C
A

Forward Primers:

5'GCTAAGCTT AAP GAP ATQ CCA GAQ GAQ TA3' Desat 13-1
A CCG Desat 13-2
CCC Desat 13-3
CCT Desat 13-4

Reverse Primers:
(complements)

Desat 13-5a 3' GTQ TGN TAC GAN TTP TGCTTAAGCGA 5'
Desat 13-6a AAQ

Oligonucleotides

P = A or G
Q = T or C
N = A, C, T or C

FIGURE 6

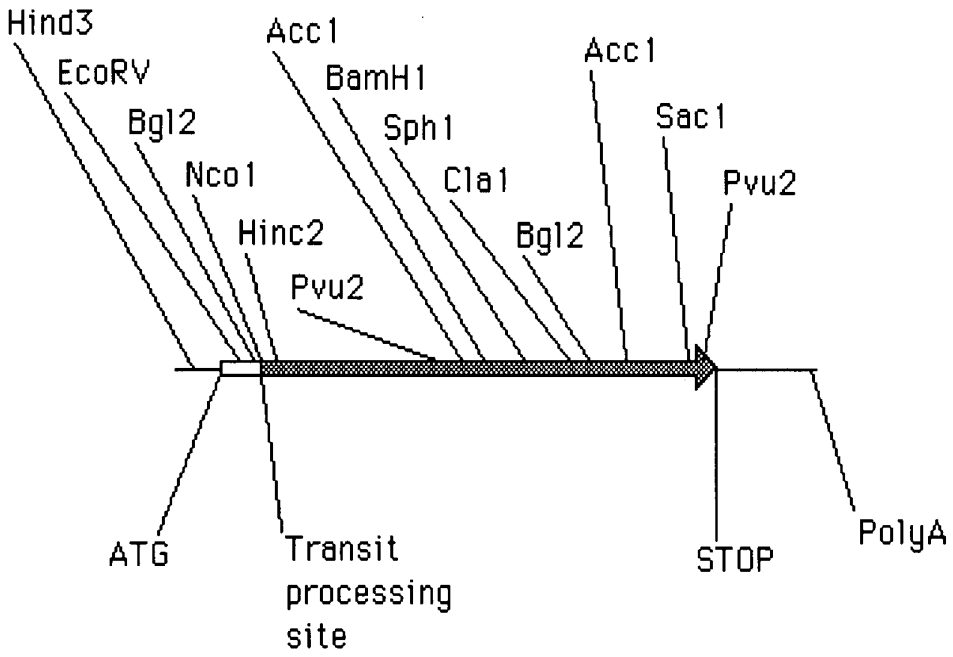

Hind3
EcoRV
Bgl2
Nco1
Hinc2
Pvu2
Acc1
BamH1
Sph1
Cla1
Bgl2
Acc1
Sac1
Pvu2
ATG
Transit
processing
site
STOP
PolyA

FIGURE 7A

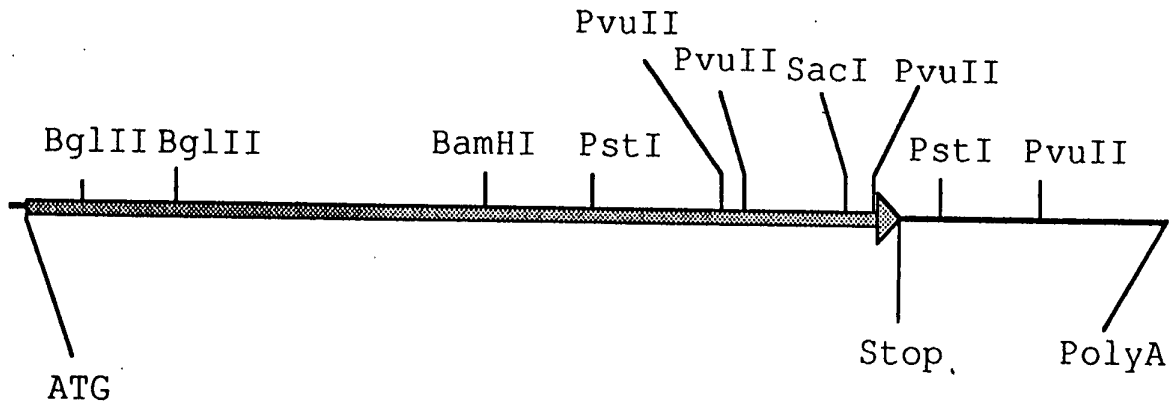

PvuII
PvuII
SacI
PvuII
BglII
BglII
BamHI
PstI
PstI
PvuII
ATG
Stop
PolyA

FIGURE 7B

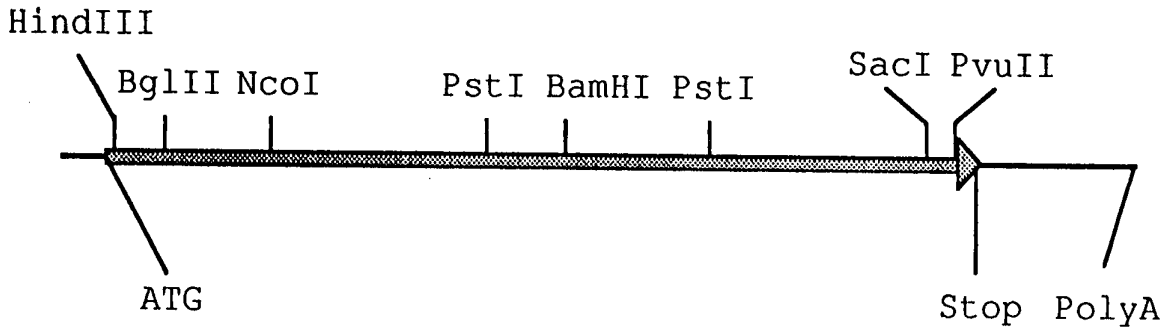

HindIII
BglII NcoI
PstI BamHI PstI
SacI PvuII
ATG
Stop PolyA

FIGURE 7C

```
TCTAGAATTC TCTAATTACG TCTGTTTGTT CTATTTTTTA TATGATATCA AATATTCGTC ATAAATATAT    70
GGTTTAAGAT GCCAAAAAAT TATTTACTTG GTGAATATAA TACGTTAAAT ATTAGAAATA CATCATTTAG   140
TTAAATAAAT AACCAAAAAC CAAAAATTCA TATCCGCGCT GGCGCGCGGT CAGGGTCTCG TTAGTTTTAA   210
AATCAATGCA GTTTACAATT AATTTCCAGC TGAAAATAAG TATAATTTGT ATTGAAATTA TAAAGTGACA   280
TTTTTTGTGT AACAAATATT TTGTGTAACA AGAATTAAAA AAAAAAACAG AAAATACTCA GCTTTTTTAA   350
TAATAAAAAA AATTAATTGA GTTAGAAAAT TGTTGTACCA ATAACAAAAG ATTTATATGG AATTATAAAA   420
TCAACACACC AATAACACAA GACTTTTTAA AAATTTAAGA ATAATATAAG CAATAACAAT AGAATCTTCA   490
AATTCTTCAA ATCCTTAAAA ATCAATCTCC CACTATTAAT CCCCCTTAGT TTTAGTTGGT AATGGCAACG   560
TTTGTTGACT ACCGTATTGT AACTTTTGTC AAATTGTCAT AAATACGTGT CAAACTCTGG TAAAAAATTA   630
GTCTGCTACA TCTGTCTTTT ATTTATAAAA CACAGCTGTT AATCAGAATT TGGTTTATTA AATCAACAAC   700
CTGCACGAAA CTTGTGTGAG CATATTTTGT CTGTTTCTGG TTCATGACCT TCTTCCGCAT GATGGCCAAG   770
TGTAATGGCC ACTTGCAAGA GCGTTTCTTC AACGAGATAA GTCGAACAAA TATTTGTCCG TTACGACCAC   840
ATATAAAATC TCCCCATCTC TATATATAAT ACCAGCATTC ACCATCATGA ATACCTCAAA TCCCAATCTC   910
ACAAATACTT CAATAAAAAG ACCAAAAAAA ATTAAAGCAA AGAAAAGCCT TCTTGTGCAC AAAAAAAAAA   980
```

FIGURE 8

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GAAGCCTTCT AGGTTTTCAC GAC ATG AAG TTC ACT ACT CTA ATG GTC ATC ACA TTG        1036
                          MET Lys Phe Thr Thr Leu MET Val Ile Thr Leu

GTG ATA ATC GCC ATC TCG TCT CCT GTT CCA ATT AGA GCA ACC ACG GTT GAA AGT      1090
Val Ile Ile Ala Ile Ser Ser Pro Val Pro Ile Arg Ala Thr Thr Val Glu Ser

TTC GGA GAA GTG GCA CAA TCG TGT GTT GTG ACA GAA CTC GCC CCA TGC TTA CCA      1144
Phe Gly Glu Val Ala Gln Ser Cys Val Val Thr Glu Leu Ala Pro Cys Leu Pro

GCA ATG ACC ACG GCA GGA GAC CCG ACT ACA GAA TGC TGC GAC AAA CTG GTA GAG      1198
Ala MET Thr Thr Ala Gly Asp Pro Thr Thr Glu Cys Cys Asp Lys Leu Val Glu

CAG AAA CCA TGT CTT TGT GGT TAT ATT CGA AAC CCA GCC TAT AGT ATG TAT GTT      1252
Gln Lys Pro Cys Leu Cys Gly Tyr Ile Arg Asn Pro Ala Tyr Ser MET Tyr Val

ACT TCT CCA AAC GGT CGC AAA GTC TTA GAT TTT TGT AAG GTT CCT TTT CCT AGT      1306
Thr Ser Pro Asn Gly Arg Lys Val Leu Asp Phe Cys Lys Val Pro Phe Pro Ser

TGT TAAATCTCTC AAGACATTGC TAAGAAAAAT ATTATTAAAA ATAAAAGAAT CAAACTAGAT      1369
Cys

CTGATGTAAC AATGAATCAT CATGTTATGG TTGAAGCTTA TATGCTGAAG TGTTTGATTT TATATATGTG  1439

TGTGTGTGTG TCCTGCTCAA TTTTTGAAAC ACACACGTTT CTCCTGATTT GGATTTAAAT TATATTTTGA  1509

GTTAAAAAAA AGAAAAAGAT GGAATGCTAT TTATACAAGT TGATGAAAAA GTGGAAGTAC AATTTAGATA  1579
```

FIGURE 8

TCTCCTACAC TTAAAGAATG AAACAATAAT AGACTTACGA AACAAATGAA AAATACATAA ATTGTCGACA 1649

ATCAACGTCC GATGACGAGT TTATTATTAA AAATTTGTGT GAAGGACTAG CAGTTCAACC AAATGATATT 1719

GAACATATAC ATCAACAAAT ATGATAATCA TAAAAGAGAG AATGGGGGGG GGGTGTCGTT TACCAGAAAC 1789

CTCTTTTTCT CAGCTCGCTA AAACCCTACC ACTAGAGACC TAGCTCTGAC CGTCGGCTCA TCGGTGCCGG 1859

AGGTGTAACC TTTCTTTCCC ATGACCCGAA ACCTCTCTTT CCCAACTCAC GAAAACCCTA CAATCAAAAA 1929

CCTAGCTCCG ACCGTCGGCT CATCGGTGCC GAAGGTGTAA CCTTTCTCTC CCATCATAGT TTCTCGTAAA 1999

TGAAAGCTAA TTGGGCAATC GATTTTTTAA TGTTTAAACC ATGCCAAGCC ATTTCTTATA GGACAATTGT 2069

CAATAATAGC ATCTTTTGAG TTTTGTCTCA AAAGTGACAC TAGAAGAAAA AAGTCACAAA AATGACATTC 2139

ATTAAAAAGT AAAATATCCC TAATACCTTT GGTTTAAATT AAATAAGTAA ACAAAAATAA ATAAAAACAA 2209

ATAAAATAAA AATAAAAAAT GAAAAAAAGA AATTTTTTTA TAGTTTCAGA TTATATGTTT TCAGATTCGA 2279

AATTTTTTAA ATTCCCTTTT TTAAATTTTC TTTTTTGAAA TTTTTTTTTT TGAAATTTTT TGAAACTGTT 2349

TTTAAAATTT TTATTTTTAA TTTTTTAGTA TTTATTTTTT ATTTTATAAA ATTTTAAACG CTAATTCCAA 2419

AACTCCCCCC CCCCCCCCCC CCCCAATTCT CTCCTAGTCT TTTTCTCTTT CTTATATTTG GGCTTCTATC 2489

TTCTCTTTTT TTTTCAGGCC CAAAGTATCA TGTGTAACAA CCGGTGTTCA AAAACGCGCC CGCCTGGCCG 2559

FIGURE 8

```
TTTACTCGCC CGATTAAATG ATGATCGGAA GGCTGCCATG GCGAGGCGGA GGTAATCAGT GGTTCTAGGC  2629
GCTGAAACTA GAAAACCTTC AAAAATCGAA ATTTTAAGAG CTAAATCGGT GTTTATCTCA TGAATCTATT  2699
ATATTTAGTT GAAACTCACA AGAATCGGTT GTAAAAACTA TGAAATCGTG CAAAAAAAAT GAAGAACAAA  2769
ATATTCTCAG ATCTGGAAAA CACAGAGAAG AGGTTGAAGA TGAGGGTAAA ATCGTATTTT GTCATTCATT  2839
AAACTAAAAT CAAAAAAAAA TGATGCAAAA TTCAATGATA ATAACTCGAA CTCGCAACCA TATGCATCTT  2909
TAGACTGCGA CACGGACCAC TAGACTAAGC AATTTTAATG TTTATTCATC ACAGACCTAA TATATGTCTA  2979
AAACTAGGCG CCGAGTACGC CCCGCTTAAT CCCGAGTTTT TGTTAGCTCG CTAGACCCAG GGTCACCGCC  3049
CGACTAACGA GTAGCGTAAT TCTGAACTGG GGTAACAACA TAGAGAACAT CGCCGACCCT TCCCTGCCGA  3119
TGATGCCGCC TCCGATGAAC TTCCTGTAAC GCCTTCAGTT TCCATTGATT TTCCCCTTTA ATCTGATCAG  3189
TTCCATGTTT TATCCAACTC ATCCCACTCC GTAGCATTTA ATCGATCTCA TCATTTACAT ACATAACCAG  3259
TAGGAGGTCT CATATAAATT TGAACGTTTC CAGCGATGAA CAGTGCCAAT CTCTGCGAAA TCCATTTCTC  3329
TAAGCTCAGG GCTGGCGGCT GCAGCCCGGG GATCCACTAG TTCTAGGCGG CCGCACCGCG GTGGAGCTCC  3399
AATTCGCCCT ATAGTGAGTC GTATTACGCG CGCTCACTGG C                                  3440
```

FIGURE 8

CTCGAGAGCT GAAGGATTTT TTGTTAGAGA TTCAACGACA GATGGACCCT TCCTCCACTA 60

GGCAACTGCA AGAACCTAAC AATGCAAATA TCACTCCTCC TCAGCCTTCA AGGAGCGTTA 120

ATAGGACTGG AACAAGCGGT CAAGTGAGTA AATTTTCCTT CCAAGATAGA TCTCTATGGT 180

TCGGTTCATG AAGTTTGTGG TTTAATTGTG TAGCAACAGG ATAGTGCAAG TGAGAATAGA 240

GTTCGACCTC ATCTACCTAC CCCGGAACCT CTGAATGTAT CCCCATTGAA GAAGAAGAGG 300

GCAAATCCTG CACCCAGAAG GATAAAGAAA TTTTGGACGC CTGAAGAAGT GGCAGTTCTG 360

AGGGAAGGAG TAAAAGAGTA TGTCTACTAC TACTACTCTA TAATCAAGTT TCAAGAAGCT 420

GAGCTTGGCT CTCACTTTAT ATGTTTGATG TTGTTGTGCA GGTATGGTAA ATCATGGAAA 480

GAGATAAAGA ATGCAAACCC TGAAGTATTG GCAGAGAGGA CTGAGGTGAG AGAGCATGTC 540

ACTTTTGTGT TACTCATCTG AATTATCTTA TATGCGAATT GTAAGTGGTA CTAAAAGGTT 600

TGTAACTTTT GGTAGGTGGA TTTGAAGGAT AAATGGAGGA ACTTGCTTCG GTAGCGGTAA 660

CAAGTTTTAT ATTGCTATGA AGTTTTTTTG CCTGCGTGAC GTATCAGCAG CTGTGGAGAA 720

GATGGTATTA GAAAGGGTCT TTTCACATTT TGTGTTGTGA CAAATATTAA TTCGGCCGGT 780

ATGGTTTGGT TAAGACTTGT TGAGAGACGT GTGGGGTTTT TTGATGTATA ATTAGTCTGT 840

GTTTAGAACG AAACAAGACT TGTTGCGTAT GCTTTTTTTA ACTTGAGGGG GTTTGTTGTT 900

GTTAGTTAGG AACTTGACTT TGTCTCTTTC TCTCAAGATC TGATTGGTAA GGTCTGGGTG 960

GTAGTACTGT TTGGTTTAAT TTGTTTTGAC TATTGAGTCA CTGTGGCCCA TTGACTTTAA 1020

FIGURE 9

ATTAGGCTGG TATATTTTTT GGTTTAAAAC CGGTCTGAGA TAGTGCAATT TCGATTCAGT 1080

CAATTTTAAA TTCTTCAAGG TAATGGGCTG AATACTTGTA TAGTTTTAAG ACTTAACAGG 1140

CCTTAAAAGG CCCATGTTAT CATAAAACGT CATTGTTTAG AGTGCACCAA GCTTATAAAA 1200

TGTAGCCAGG CCTTAAAAGA CTTAACAGGC CTTAAAAGAC TTAACATTCC TTAAAAGGCC 1260

CATGTTATCA TAAAACGTCA TCGTTTTGAG TGCACCAAGC TAAATGTAGC CAGGCCTTAA 1320

AAGACTTAAC AGGCCTTAAA AGGCCCATGT TATCATAAAA CGCCGTCGTT TTGAGTGCAC 1380

CAAGCTTATA AATGTAGCCA GCTACCTCGG GACATCACGC TCTTTGTACA CTCCGCCATC 1440

TCTCTCTCTC TCGAGCAGAT CTCTCTCGGG AATATCGACA ATGTCGACCA CTTTCTGCTC 1550

TTCCGTCTCC ATGCAAGCCA CTTCTCTGGT AATCTCATCT CCTTCTTGTG TTCCCAGATC 1560

GCTCTGATCA TACTTTCTTT TAGATCATTT GCCTCTGATC TGTTGCTTGA TGTTTGTTAA 1620

CTCTCCACGC ATGTTTGATT ATGTTGAGAA TTAGAAAAAA AATGTTAGCT TTACGAATCT 1680

TTAGTGATCA TTTCAATTGG ATTTGCAATC TTGTGTGACA TTTGAGGCTT GTGTAGATTT 1740

CGATCTGTAT TCATTTTGAA TCACAGCTAT AATAGTCATT TGAGTAGTAG TGTTTTTAAA 1800

TGAACATGTT TTGTTGTATT GATGGAACAA ACAGGCAGCA ACAACGAGGA TTAGTTTCCA 1860

GAAGCCAGCT TTGGTTTCAA CGACTAATCT CTCCTTCAAC CTCCGCCGTT CAATCCCCAC 1920

TCGTTTCTCA ATCTCCTGCG CGGTATGTTC TCATTCTCAG CATTTATTTC GAGCTTGCTT 1980

GTCATGGTAC TCTCTCTAAT TGTCTATTTG GTTTATTAGG CCAAACCAGA GACGGTTGAG 2040

FIGURE 9

AAAGTGTCTA AGATAGTTAA GAAGCAGCTA TCACTCAAAG ACGACCAAAA GGTCGTTGCG 2100

GAGACCAAGT TTGCTGATCT TGGAGCAGAT TCTCTCGACA CTGTAAGTCA TCAATCATTC 2160

TCTTATGTGA ATAAAGAGAA CTTGAAGAGT TTGTTTTTAA CATATTAACT GAGTGTTTTG 2220

CATGCAGGTT GAGATAGTGA TGGGTTTAGA GGAAGAGTTT GATATCGAAA TGGCTGAAGA 2280

GAAAGCTCAG AAGATTGCTA CTGTGGAGGA AGCTGCTGAA CTCATTGAAG AGCTCGTTCA 2340

ACTTAAGAAG TAATTTTAGT ATTAAGAGCA GCCAAGGCTT TGTTGGGTTT GTTGTTTTCA 2400

TAATCTTCCT GTCATTTTCT TTTTCTTTAA TGTGTCAAGC GACTCTGTTG GTTTAAAGTA 2460

GTATCTGTTT GCCATGGATC TCTCTCTATT TGTCGACTGA AAACTTTTGG TTTACACATG 2520

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ATTAACACAT ACATAAGTCA AAGAGTAGGC CCTAAGATGA CAATTTATAA ACAATCCTAT 2640

TCACATTGTA TATACAGGTT ATGATTATTC CCAATCAGCG TCAAAGAATC CAGCATCTTT 2700

CATCTCTGAA TAGTAGACAT TCTCCAAGTT CACATCTTCC TCCTGCACCA AAAACCAGTA 2760

CTAAATCATG AACATTGCAA TAATCACATG CCTAGGCGAG AGTTTTGGTG ATGTGGTGTT 2820

AGTGATAGTG ATACTGATGG TGCTAGAGCG GTTAAGAAGG ATTAACCTGG AAGAAGTCTG 2880

CAAGGAAAGT AACATAGAGA AGAGGAAGAT AGGAGTGGTA ACAAACACTT GTGATCCCAT 2940

ACAGCCTCCC AGCATTTTTC AAATGTTATT TCCTTACATA AAGAAACAAG AGAAGTCTGA 3000

CTAGATGATA TTTATATAGG ATAAGTGTTT TACCATAAGC CAAAGTGAGC GCCGTTTGCA 3060

FIGURE 9

AGAGCTAACC AGACAGTACA CGTTTGGCAT ATATCTCATC AACATGATCT GAAAAGTAAC 3120

ATATCACAGT TAATGAACAC AATGGTTACC TTGAGAAGCA AATCAAGACC TATAACAAGC 3180

CCAGAGATGA GGAAAGTCCG TGTCAACGCT TCACCGCCAT TCGCGTAGTT TCCTTGGAAG 3240

ACAAAGGCCA CCAACCAAAC TTACTTCCAG AAACAACACT CCAAATGTTG TCAACAAAGT 3300

CAATAGATTC CAAACTACTT CGTTACAGGG TTGTATAGAT AATATAATAG AATAGTGGGA 3360

AGATAGTATA AATAAAATAA ATAAAAGATC CTATCGGTAA ATAGTTTATA ATATCGGGGG 3420

CGTATATAAA GTATAAAAGA AACTCTTCTC CAATCCGACC GTTGAAAATC ACTCTCAATC 3480

TCTGGCGTAA CGACCGGATC GTTCGCGCGT AATTTTCGCT GCTATAAATA GAAACTTTCC 3540

TCTTCTGTTT CTCGATCAAA ATTTTTTTTT GGAAAAATTA AGTTTGAATC TATCGTAGAT 3600

GCTGTGACAA AAAAAAATTG TTTTATCGAA GATGAGAAAC ATGAGGCCTG TTCATGCAAG 3660

GAACCAGACC ACGGATCCAT CTTCGCCGAT GATGACGTCT CCTCTGATGA ATCGTCACGC 3720

ACGGACAGGA TCCAACGCTG GACCAGCATC TAACGCCAAG AAAGCACAGA CGAAAGCAGC 3780

AGCTCAGAGA CTCGCGGCTG TGATGTCGAA CCAAACAGGC GACGATGAAG ACAGTGATGA 3840

TGACCTTTCC TTTGACTACA ACGCTGTCGG AAGCATTGGT CTCGCTGCCG GAAGATCT 3898

FIGURE 9

Lambda CGN1-2

NCG-186 Linear LENGTH = 4325

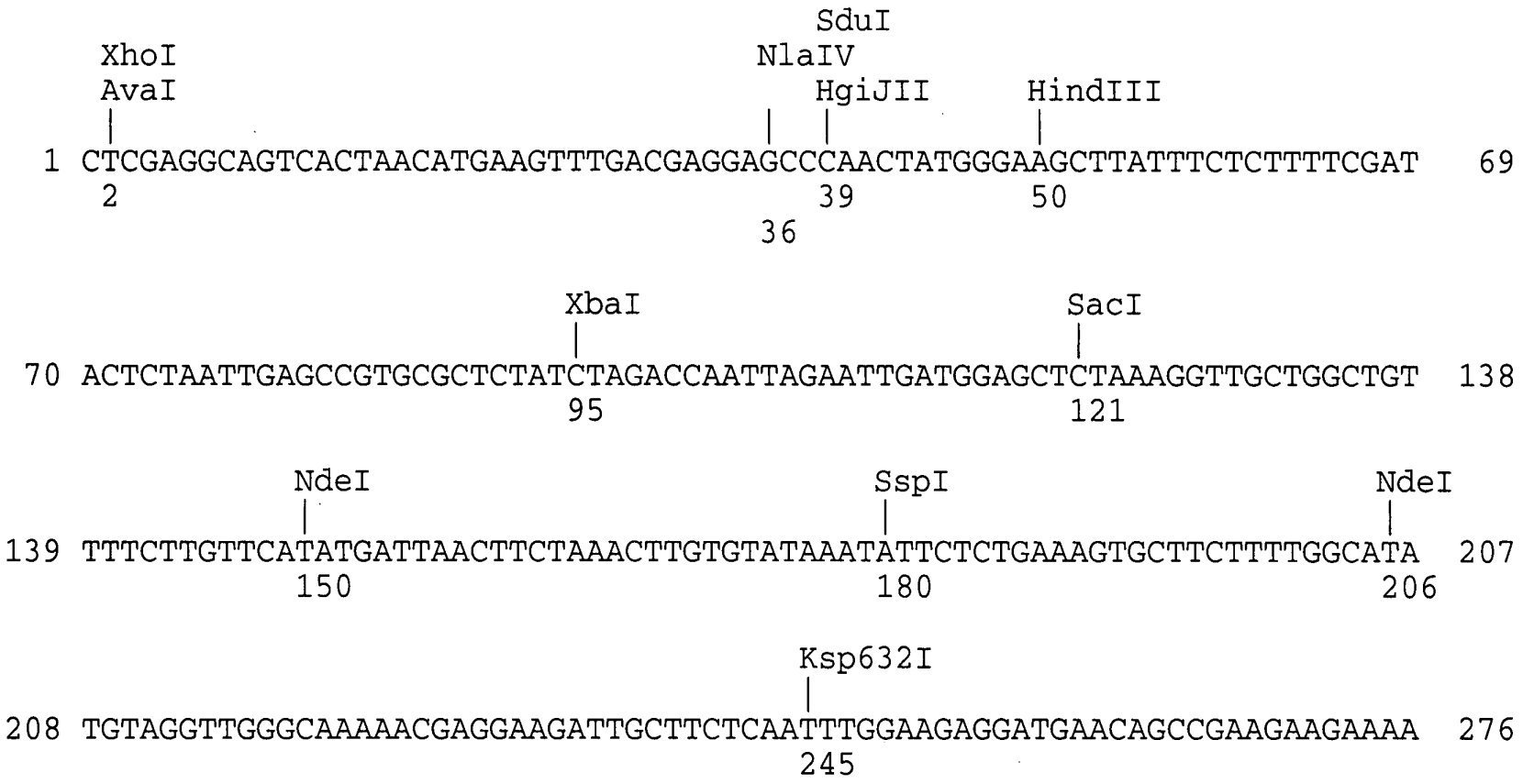
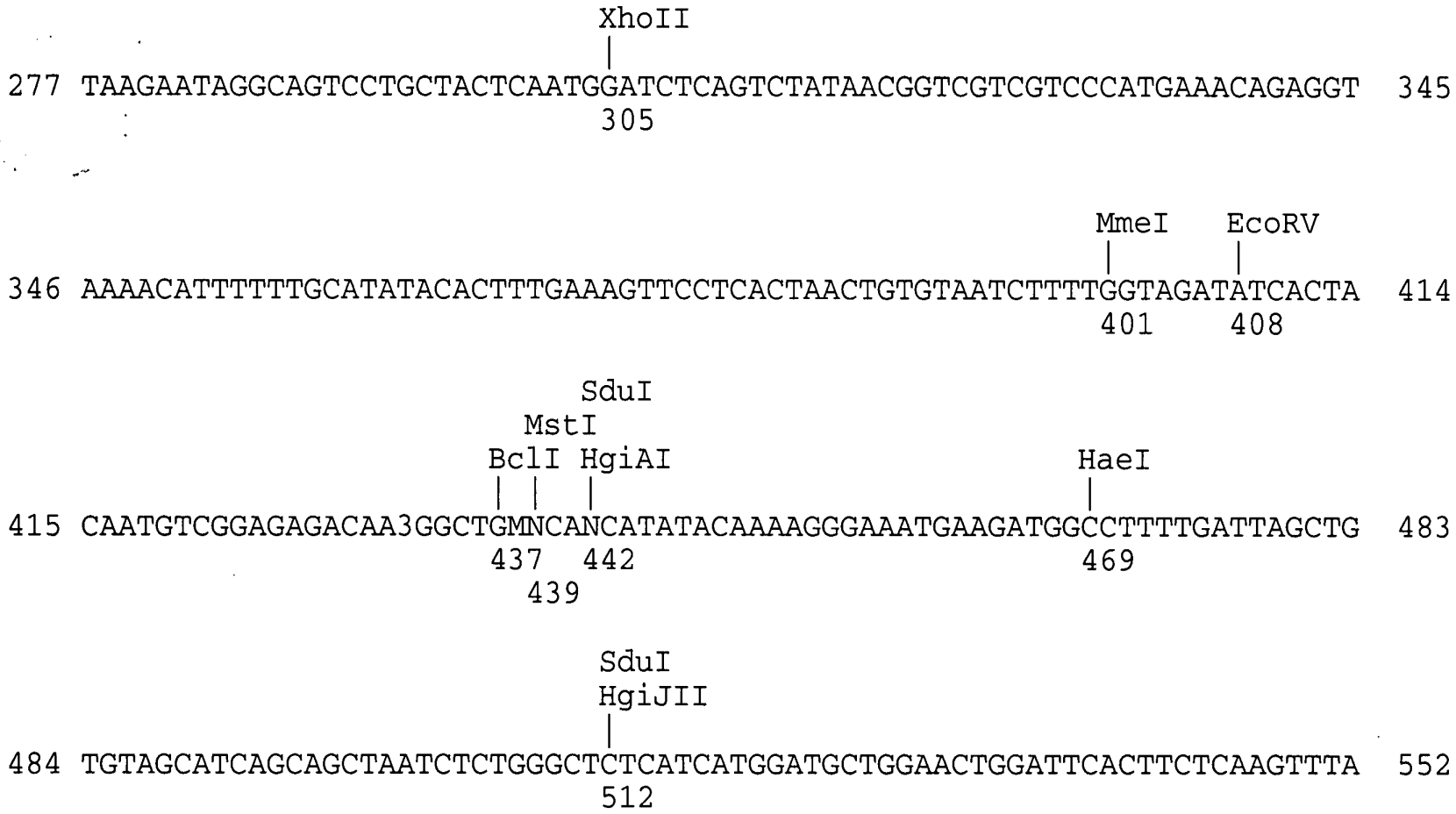


FIGURE 10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MmeI
EcoRV
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401
408
SduI
MstI
BclI
HgiAI
HaeI
415 CAATGTCGGAGAGACAA3GGCTGMNCANCATATACAAAAGGGAAATGAAGATGGCCTTTTGATTAGCTG 483
437
442
469
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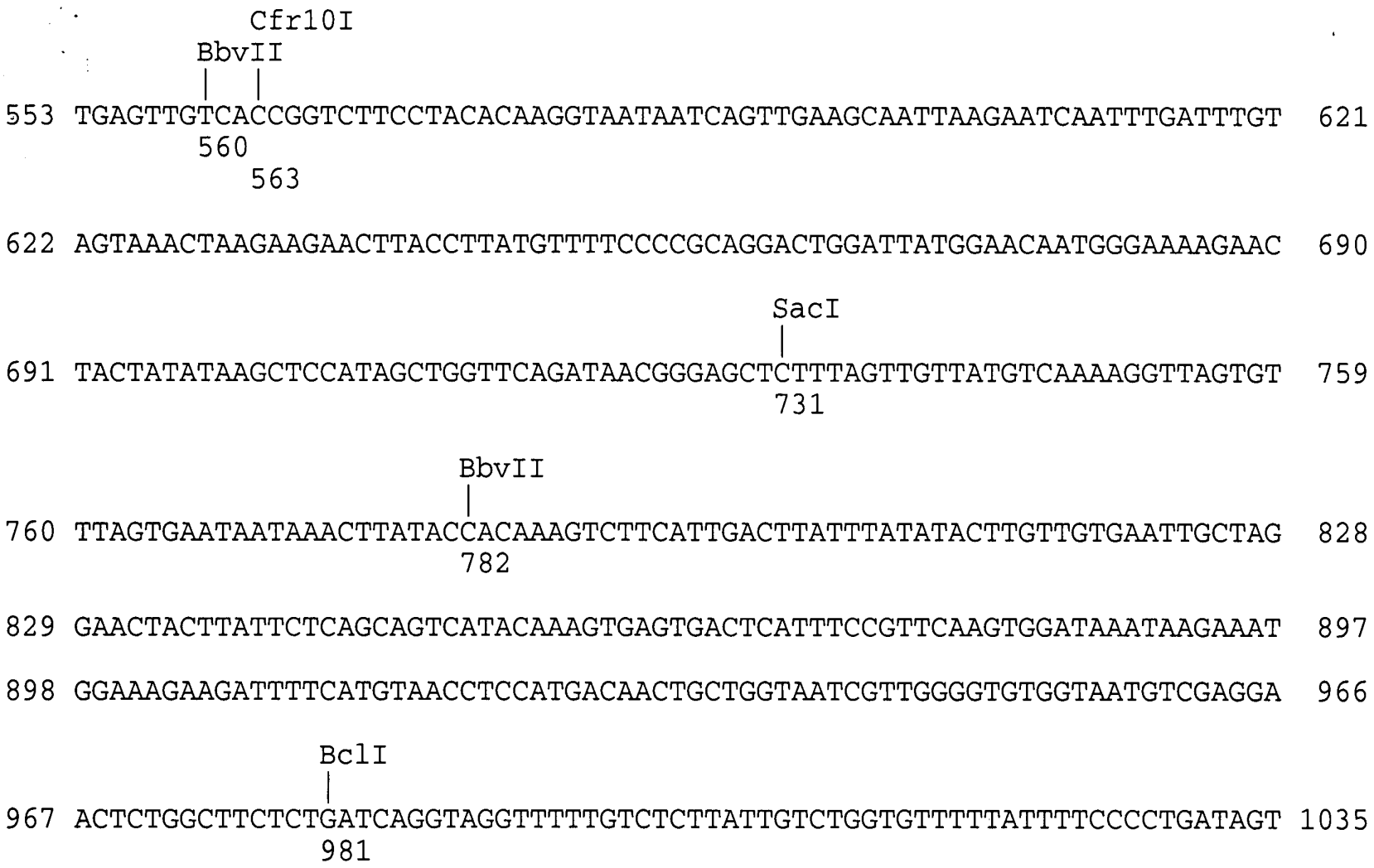
HgiJII
484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA 552
512

FIGURE 10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BbvII
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SacI
691 TACTATATAAGCTCCATAGCTGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT 759
731
BbvII
760 TTAGTGAATAATAAACTTATACCACAAAGTCTTCATTGACTTATTTATATACTTGTTGTGAATTGCTAG 828
782
829 GAACTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT 897
898 GGAAAGAAGATTTTCATGTAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGGA 966
BclI
967 ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTTATTTTCCCCTGATAGT 1035
981

FIGURE 10


1036 CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTTGTACCCAAGCGATGGGATAC 1104
1105 ATAGGAGGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATAT 1173
Tth111II
ScaI
1174 TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAGTA 1242
1175
1242
XhoII
1243 CTCATGTCAAGGTTGGTTTCTTTAGCTTTGAACACAGATTTGGATCTTTTTGTTTTGTTTCCATATACT 1311
1285
1312 TAGGACCTGAGAGCTTTTGGTTGATTTTTTTTTCAGGACAAATGGGCGAAGAATCTGTACATTGCATCA 1380
AflII
1381 ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAGCATCATGTGGAAAGCCAAAGACAATTGGAG 1449
1415
1450 CGAGACTCAGGGTCGTCATAATACCAATCAAAGACGTAAAACCAGACGCAACCTCTTTGGTTGAATGTA 1518
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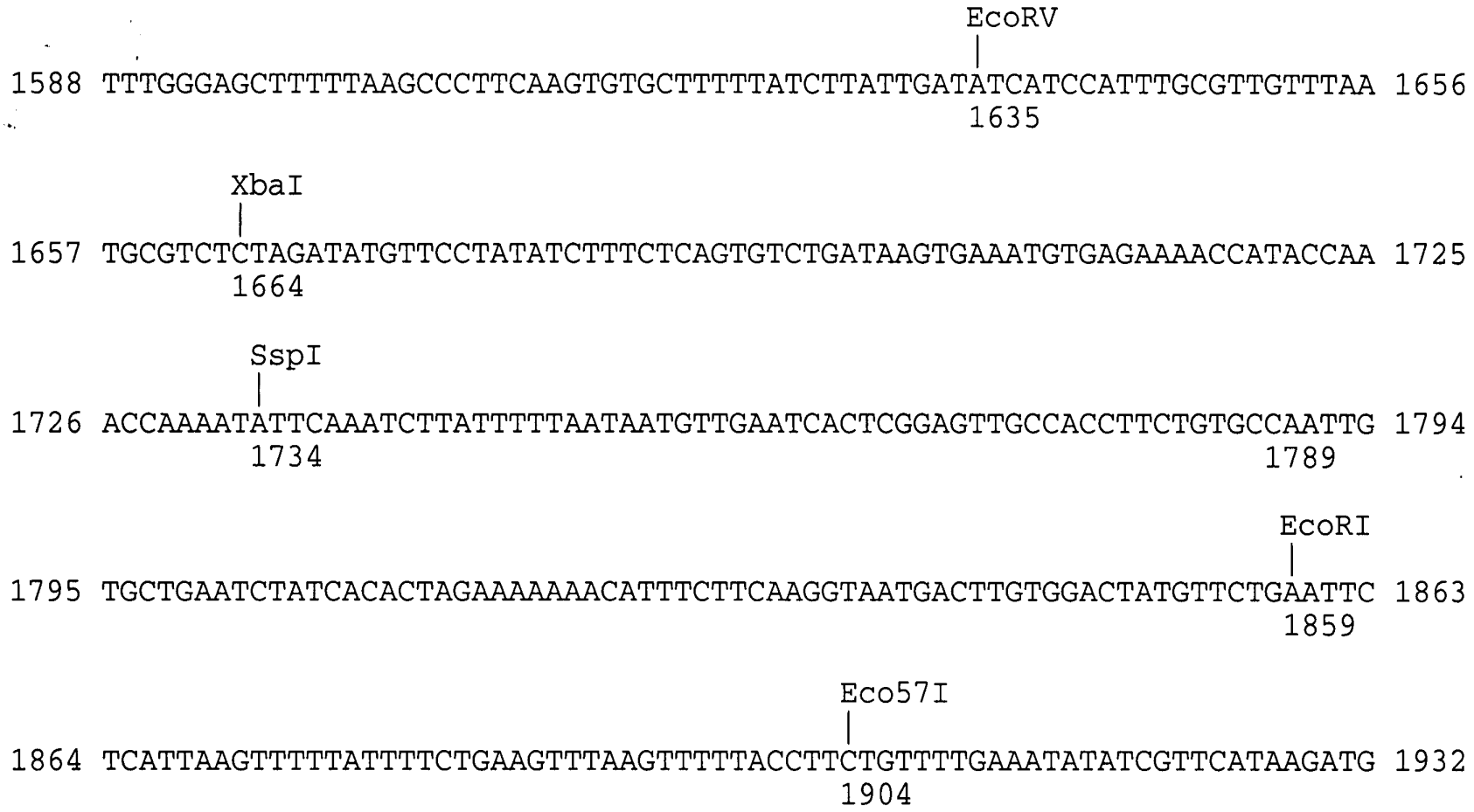
1587

FIGURE 10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1664
SspI
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1734
1789
EcoRI
1795 TGCTGAATCTATCACACTAGAAAAAAACATTTCTTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC 1863
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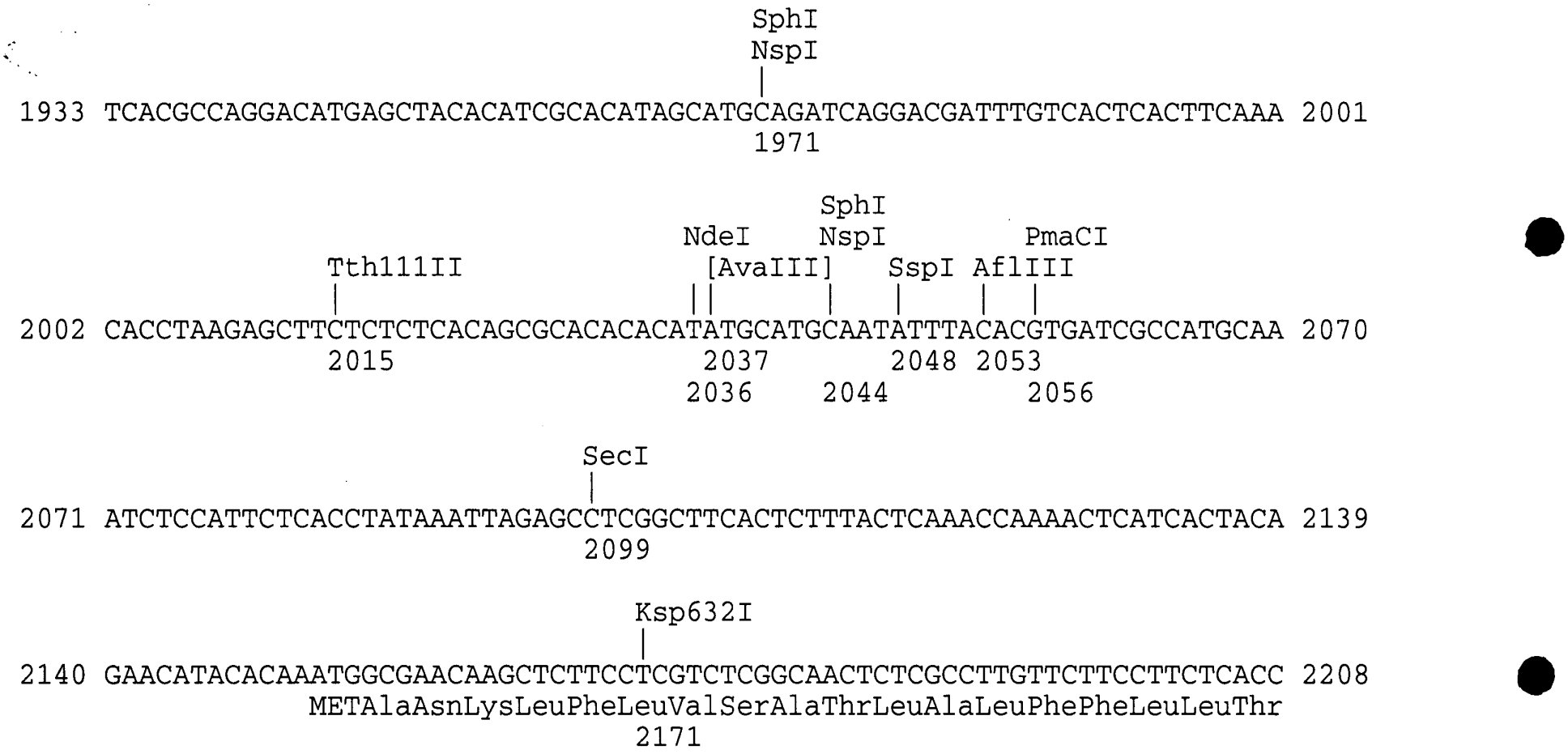
FIGURE 10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NspI
1933 TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTTGTCACTCACTTCAAA 2001
1971
SphI
NdeI NspI PmaCI
Tth111II [AvaIII] SspI AflIII
2002 CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCAATATTTACACGTGATCGCCATGCAA 2070
2015 2037 2048 2053
2036 2044 2056
SecI
2071 ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAACCAAAACTCATCACTACA 2139
2099
Ksp632I
2140 GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTTCTTCCTTCTCACC 2208
METAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPhePheLeuLeuThr
2171

FIGURE 10


SalI
HindII
NaeI
AccI
AccI
Cfr10I
2209 AATGCCTCCGTCTACAGGACGGTTGTGGAAGTCGACGAAGATGATGCCACAAATCCAGCCGGCCCATTT 2277
AsnAlaSerValTyrArgThrValValGluValAspGluAspAspAlaThrAsnProAlaGlyProPhe
2220
2241
2267
2242
2269
2240
Tth111II
HindIII
NlaIV
2278 AGGATTCCAAAATGTAGGAAGGAGTTTCAGCAAGCACAACACCTGAAAGCTTGCCAACAATGGCTCCAC 2346
ArgIleProLysCysArgLysGluPheGlnGlnAlaGlnHisLeuLysAlaCysGlnGlnTrpLeuHis
2325
2342
Tth111II
NlaIV
BbvII
2347 AAGCAGGCAATGCAGTCCGGTAGTGGTCCAAGCTGGACCCTCGATGGTGAGTTTGATTTTGAAGACGAC 2415
LysGlnAlaMETGlnSerGlySerGlyProSerTrpThrLeuAspGlyGluPheAspPheGluAspAsp
2363
2384
2415
NlaIV
SacI
ApaI
GsuI
HaeI
NspBII
Ksp632
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ValGluAsnGlnGlnGlnGlyProGlnGlnArgProProLeuLeuGlnGlnCysCysAsnGluLeuHis
2438
2444
2449
2455
2481
2436
2484

FIGURE 10


2485 CAGGAAGAGCCACTTTGCGTTTGCCCAACCTTGAAAGGAGCATCCAAAGCCGTTAAACAACAGATTCGA 2553
GlnGluGluProLeuCysValCysProThrLeuLysGlyAlaSerLysAlaValLysGlnGlnIleArg
2554 CAACAACAGGGACAACAAATGCAGGGACAGCAGATGCAGCAAGTGATTAGCCGTATCTACCAGACCGCT 2622
GlnGlnGlnGlyGlnGlnMETGlnGlyGlnGlnMETGlnGlnValIleSerArgIleTyrGlnThrAla
SecI
BbvII
2623 ACGCACTTACCTAGAGCTTGCAACATCAGGCAAGTTAGCATTTGCCCCTTCCAGAAGACCATGCCTGGG 2691
ThrHisLeuProArgAlaCysAsnIleArgGlnValSerIleCysProPheGlnLysThrMETProGly
2684
2687
NlaIV
HgiJII
ApaI
XhoI
AvaI
SecI
DsaI
AccI
2692 CCCGGCTTCTACTAGATTCCAAACGAATATCCTCGAGAGTGTGTATACCACGGTGATATGAGTGTGGTT 2760
ProGlyPheTyr .
2694
2724
2736
2692
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2774

FIGURE 10

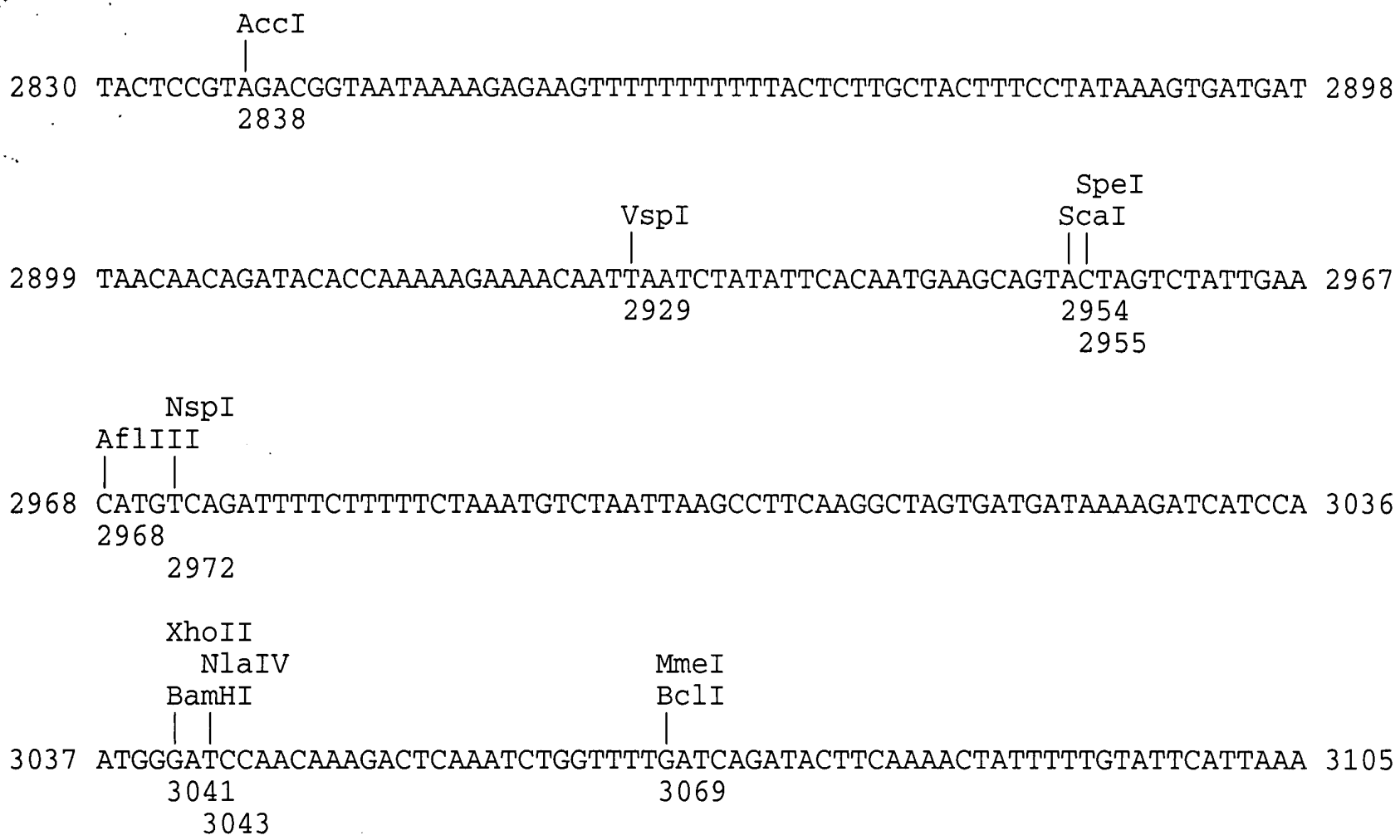
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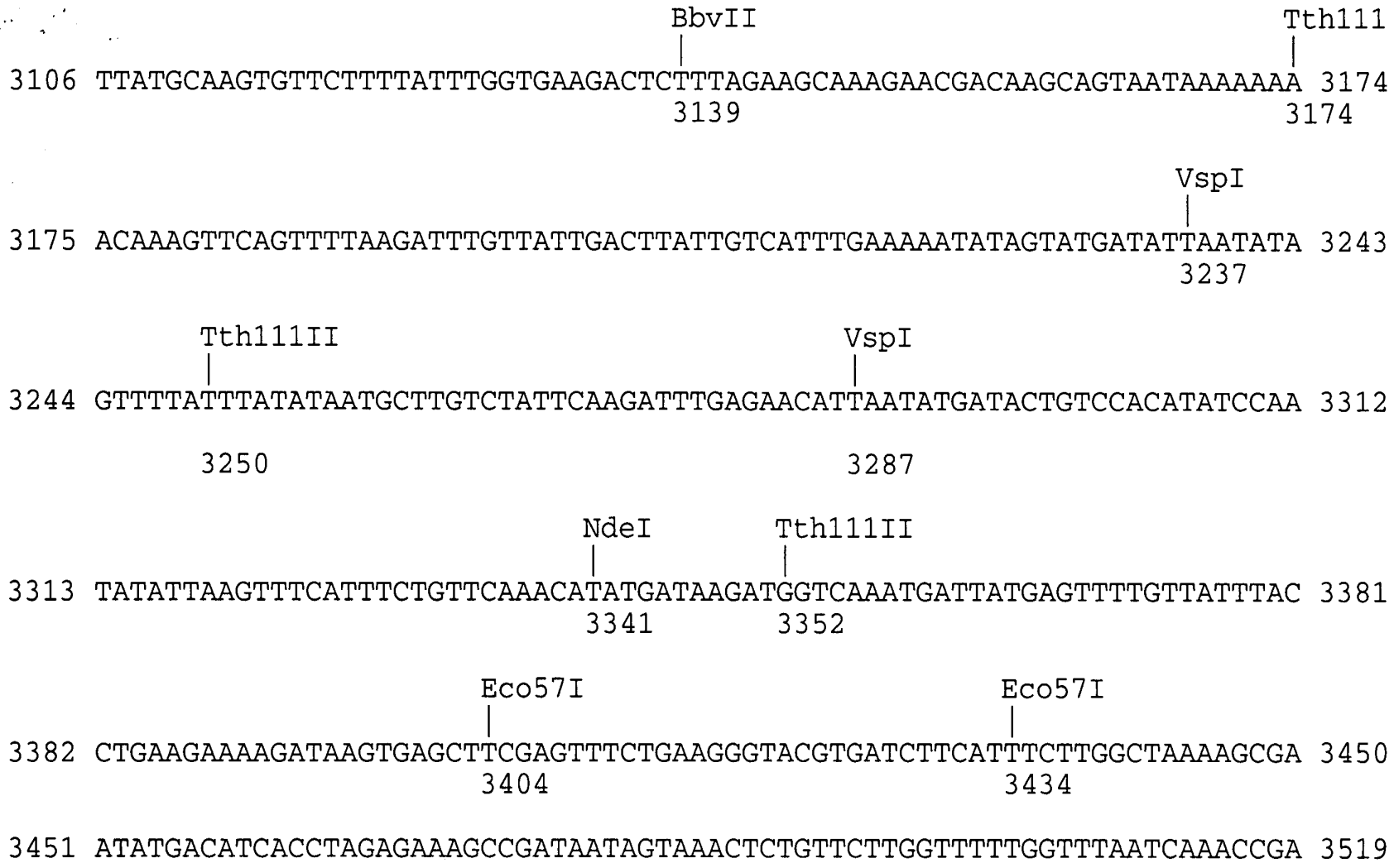
FIGURE 10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VspI
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3250
3287
NdeI
Tth111II
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3341
3352
Eco57I
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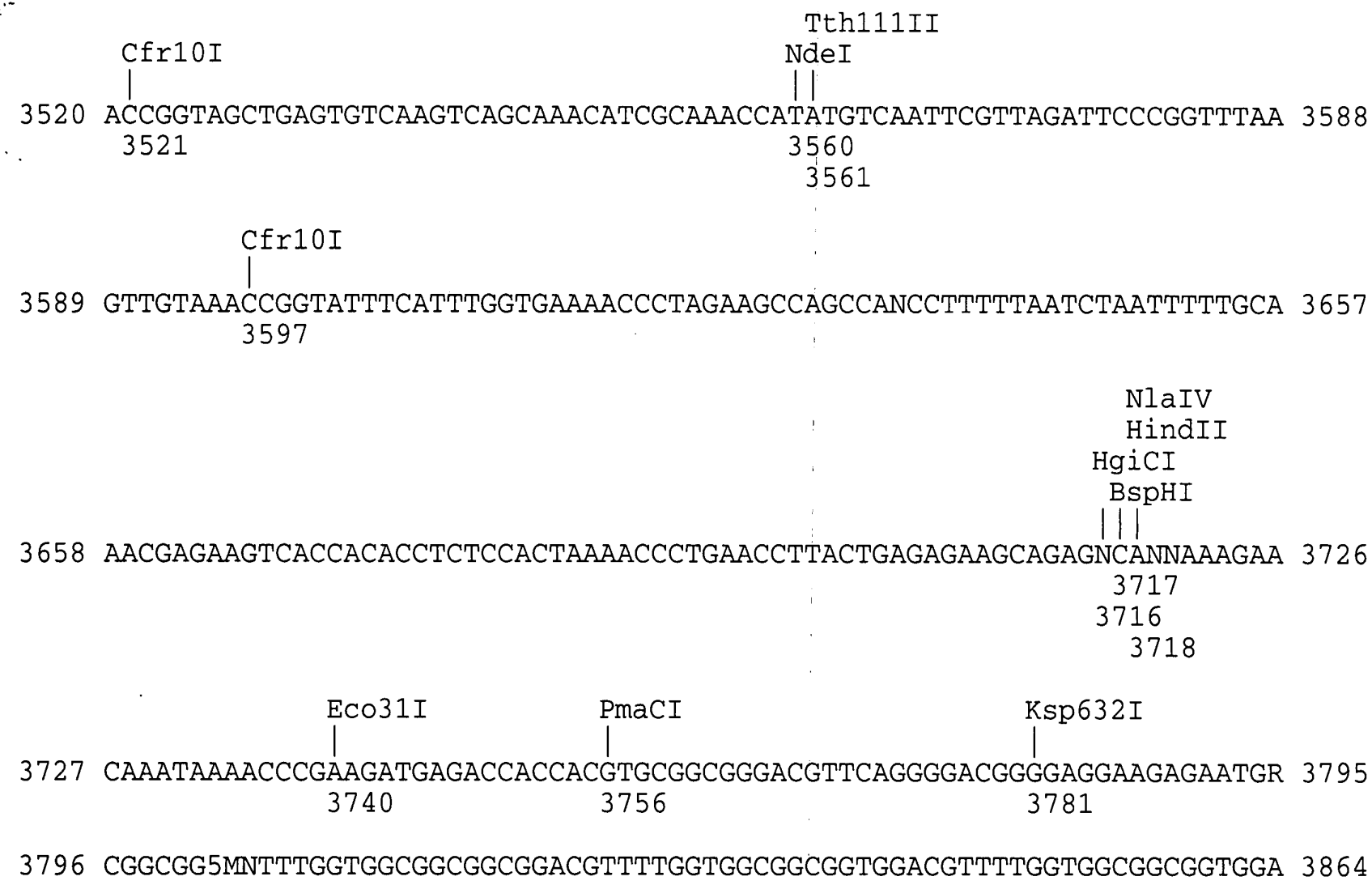
FIGURE 10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3561
Cfr10I
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3597
NlaIV
HindII
HgiCI
BspHI
3658 AACGAGAAGTCACCACACCTCTCCACTAAAACCCTGAACCTTACTGAGAGAAGCAGAGNCANNAAAGAA 3726
3717
3716
3718
Eco31I
PmaCI
Ksp632I
3727 CAAATAAAACCCGAAGATGAGACCACCACGTGCGGCGGGACGTTCAGGGGACGGGGAGGAAGAGAATGR 3795
3740
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3796 CGGCGG5MNTTTGGTGGCGGCGGCGGACGTTTTGGTGGCGGCGGTGGACGTTTTGGTGGCGGCGGTGGA 3864

FIGURE 10

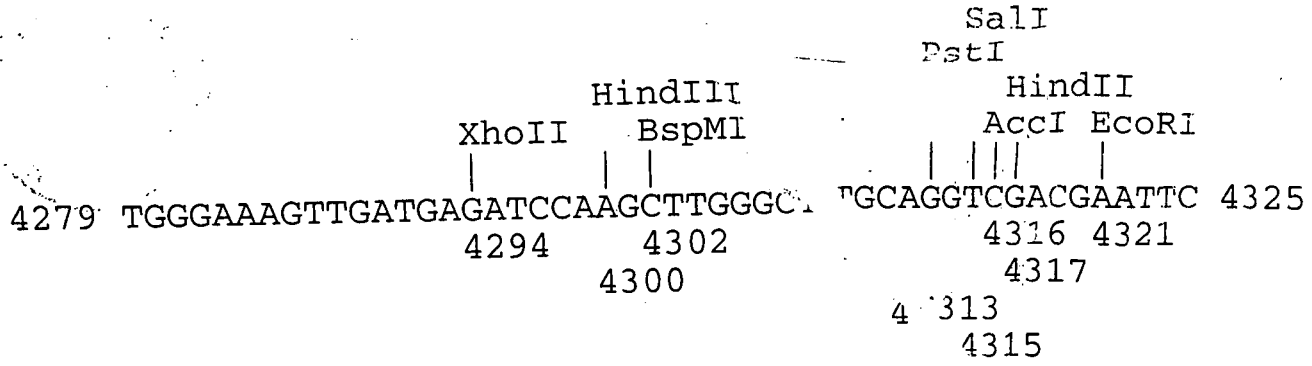

FIGURE 10
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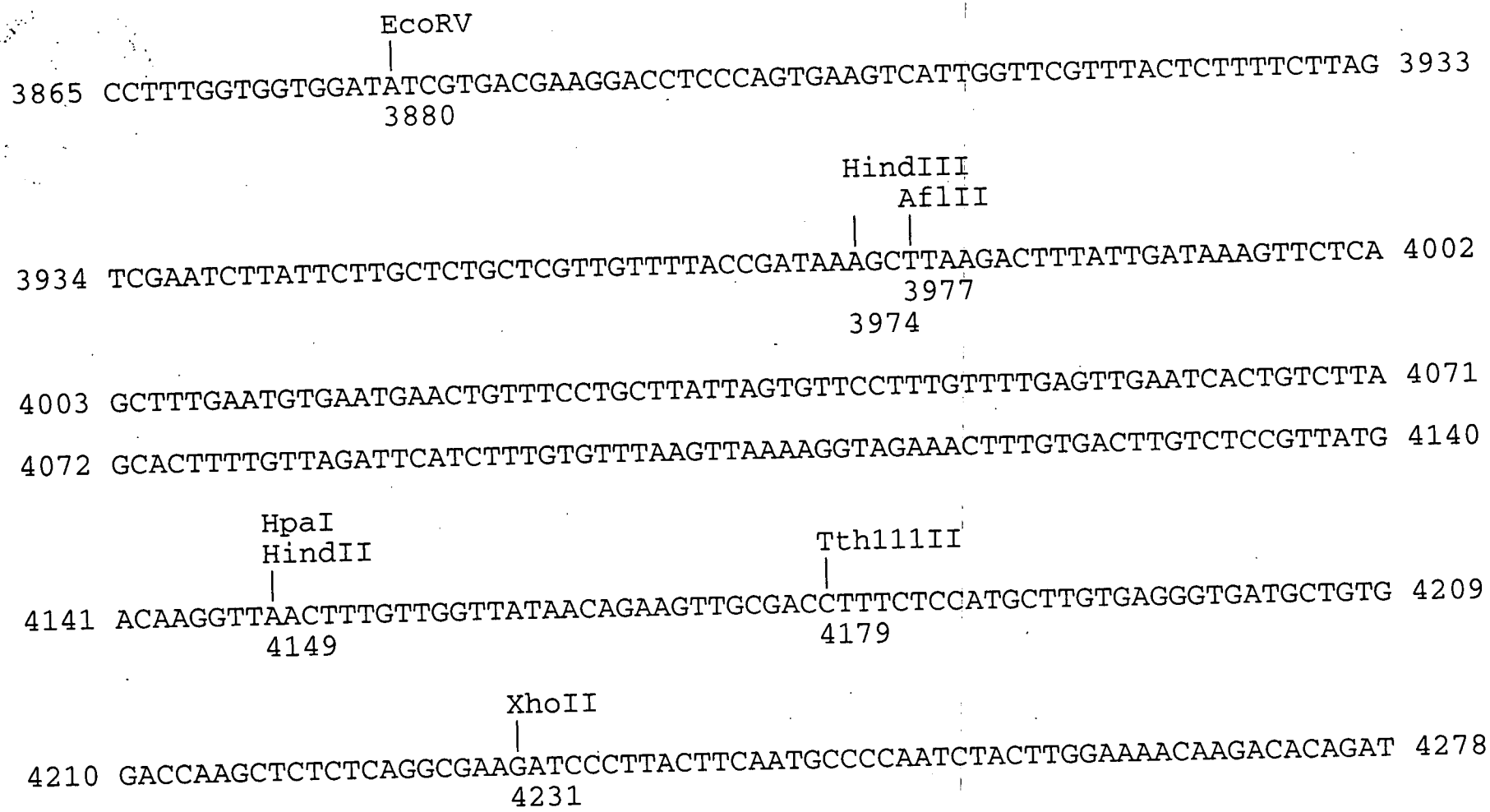
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3977
3974
4003 GCTTTGAATGTGAATGAACTGTTTCCTGCTTATTAGTGTTCCTTTGTTTTGAGTTGAATCACTGTCTTA 4071
4072 GCACTTTTGTTAGATTCATCTTTGTGTTTAAGTTAAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG 4140
HpaI
HindII
Tth111II
4141 ACAAGGTTAACTTTGTTGGTTATAACAGAAGTTGCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG 4209
4149
4179
XhoII
4210 GACCAAGCTCTCTCAGGCGAAGATCCCTTACTTCAATGCCCCAATCTACTTGGAAAACAAGACACAGAT 4278
4231

FIGURE 10